

ABSTRACT OF THE DISCLOSURE

The present invention provides a method for graphically indicating a correspondence between cDNA and genome sequences having an exon-intron structure to be understood easily. From search results of the similarity between a cDNA and a genome, information on the base positions of both edges of similar subsequence pairs (exon), the similarity value thereof, etc. is extracted. From such information, information on subsequence pairs determined unlikely to be significant in view of the similarity value, base length, etc., is eliminated. Furthermore, the conformity of orientation and order between exons is examined, and only an exon covering the cDNA by not less than a qualified ratio and whose correspondence to the cDNA is clear is selected. The selected exon is indicated by a segment on a graph by locating a base position on the genome sequence to an axis 1 and a base position on the cDNA sequence to another axis of the graph, thereby confirming the intron-exon structure visually as a line of segments.